Supplementary Material

Whole genome sequencing details

Whole-genome libraries for NGS were prepared with the Nextera XT kit (Illumina, San Diego, CA, USA), and sequencing was performed with 2x250-bp paired-end reads on the Illumina MiSeq. Quality control of NGS sequencing run was performed by the Bioinformatic Unit using FastQC v0.11.8 and Trimmomatic v.0.33.

We generated a C. diphtheriae and C. ulcerans cg-MLST scheme, defining specific target loci for whole-genome sequencing data typing, by using the default options of the SeqSphere+ target definer tool (Ridom, Munster, Germany). As reference we used the genome of strain NC 13129 from the National Center for Biotechnology Information (NCBI) (accession number no. BX248353.1/NC 002935.2) for C. diphtheria and the genome of strain NC 017317.1 for C. ulcerans. We included all 23 complete C. diphtheriae available from NCBI as guery sequences (accession nos. NC_016782.1, NC_016783.1, NC_016785.1, NC_016786.1, NC_016787.1, NC_016788.1, NC_016789.1, NC_016790.1, NC_016799.1, NC_016800.1, NC_016801.1, NZ_CP020410.2, NC 016802.1, NZ CP018331.1, NZ_CP025209.1, NZ_CP029644.1, LT 990688.1, NZ LR134538.1, NZ LR1345537.1, NZ CP039523.1, CP038789.1, NZ CP039522.1, and NZ CP039523.1) and 16 complete C. ulcerans available from NCBI as NC 015683.1, NC 0108101.1, NZ CP009500.1, query sequences (accession nos. NZ_CP009583.1, NZ_CP009622.1, NZ_CP009716.1, NZ_CP011095.1, NZ_CP011913.1, NZ_CP010818.1, NZ_CP021417.1, NZ_LT906443.1, NZ_LS483400.1, NZ_LS483416.1, NZ_AP019662.1, NZ_AP019663.1, and NZ_CP046863.1). The complete genome of strain NC_CPO25209.1 was used to exclude horizontally transferred genes to prevent their inclusion in the cgMLST typing scheme.

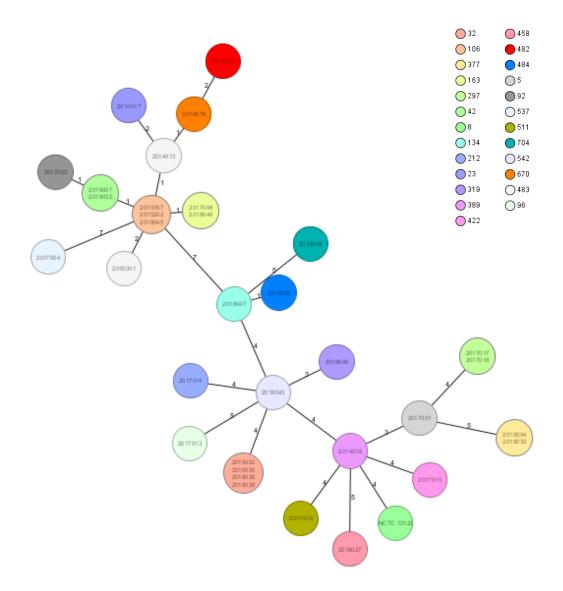


Fig. S1 - Minimum spanning tree of the clonal analysis of the *C. diphtheriae* isolates generated using the eBURST algorithm. Isolates color coded according to the eBURST group in which they were allocated on pubMLST.

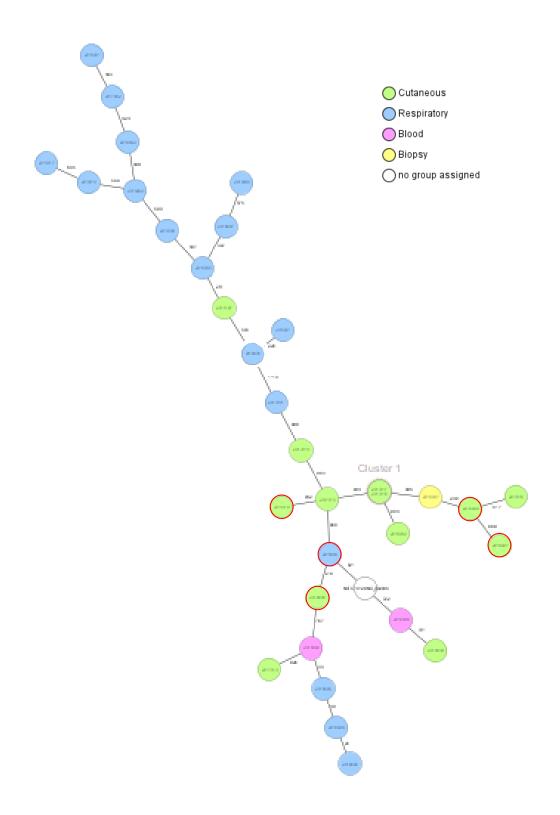


Fig. S2 - Minimum spanning tree of *C. diphtheriae* isolates generated using a cluster distance threshold of \leq 5 alleles. Colour coded according to the site of infection as indicated and all toxigenic isolates are marked with a solid red circle. The reference genome NC 13129 is white.

In silico antimicrobial resistance determinants

ResFinder analysis identified a total of 38 resistance genes with two or more resistance genes in 26% (10/39) of the isolates, all of which were identified in the C. diphtheriae isolates. Three of the toxigenic isolates harbored resistance determinants; one harbored aminoglycoside resistance genes (aadA1/aph(3")-lb/aph(3")-la/aph(6)-id), chloramphenicol resistance genes (cmx/cmlA1), a sulphonomide resistance gene (sul1) and a trimethoprim resistance gene (dfrA15). The second toxigenic isolate harbored aminoglycoside resistance genes (aph(3")-lb/aph(3")-la/aph(6)-id), a chloramphenicol resistance gene (cmx), a sulphonomide resistance gene (sul1) as well as the tetracycline resistance gene tet(33). The third toxigenic isolate harboring resistance genes to aminoglycosides (aadA5), a sulphonomide resistance gene (sul1) as well as a trimethoprim resistance gene (dfrA1). 13% (5/39) of the isolates harbored at least one aminoglycoside resistance gene, 8% (3/39) harbor at least one chloramphenicol resistance gene, 26% (10/39) harbour the sulphonamide resistance gene sul1, 18% (7/39) harbour a tetracycline resistance gene and 13% (5/39) harbored a trimethoprim resistance gene.

| isolate information | | tox status wetlab | | mo | obile elemen | t details | GC cc | ontent | | | | | detected prophage regions (PHASTER results) | | | detected PAI region coordinates | | | | | | | | | |
|-------------------------------|----------------------------------|----------------------|----------------------|-----------------------------------|--------------------------------------|----------------------------------|---------------------------|---|---------------------------------|--------------------------------|---------------------------|-------------------------|---|--|---|---|-------------|------------------------------|---------------|---|----------------------|--|---------------------------------------|----------|--|
| | | | | | | | | | | | | | | | | | start of | start of hyp. | | | start of hyp. | start of hyp. | start of | | |
| sample name | species | tox PCR | Elek | phage/PAI tox gene surrounding | length phage / PAI region [kb] | region type | genome assembly GC% | prophage / proph PAI GC % complet | prophage compleness score | prophage #Total Proteins | prophage- region_start | prophage- region_end | prophage region: most common phage | prophage results: URL | start of tRNA- Arg (acg) - 6 kb 5' of tox | start of phage integrase similar to AKN76028 | alternative | prot. with HTH a- DNA bi- | prot. similar | start of hyp. prot. similar to AKN76032 | prot. with DUF955 | prot. with HTH motif, similar to | putative transposase similar to | | |
| | | | | | | | | | | | | | | 4 | | | BAM26371 | | | | AKN76033 | AIU29548 | AKN76035 | | |
| 2014013 | C. belfantii | negative | na | no | 6,7 | prophage | 53,8% | 55,1% incomplet | e 10 | 8 | 38.787 | 45.556 | PHAGE_Gordon_Schwabeltier_NC_031255(1) | https://phaster.ca/submissions/ZZ_e333024d58 | na | na | na | na | na | na | na | na | na | na | |
| 2014013 | C. belfantii | negative | na | no | 10,9 | prophage | 53,8% | 56,0% incomplet | e 10 | 15 | 35.872 | 46.837 | PHAGE_Escher_D108_NC_013594(1) | https://phaster.ca/submissions/ZZ_e333024d58 | na | na | na | na | na | na | na | na | na | na | |
| 2014013 | C. belfantii | negative | na | no | 6,3 | prophage | 53,8% | 59,0% incomplet | e 20 | 7 | 3.799 | 10.167 | PHAGE_Gordon_Blueberry_NC_030943(2) | https://phaster.ca/submissions/ZZ_e333024d58 | na | na | na | na | na | na | na | na | na | na | |
| 2014013 | C. belfantii | negative | na | no | 7,3 | prophage | 53,8% | | | 13 | 1 | 7.308 | | https://phaster.ca/submissions/ZZ_e333024d58 | na | na | na | na | na | na | na | na | na | na | |
| 2014017 | C. belfantii | negative | na | no | 10,9 | prophage | 53,8% | | e 10 | 15 | 273 | 11.239 | PHAGE_Escher_D108_NC_013594(1) | https://phaster.ca/submissions/ZZ_2f32f5ed66 | na | na | na | na | na | na | na | na | na | na | |
| 2014017 | C. belfantii | negative | na | no | 6,8 | prophage | 53,8% | | e 10 | 8 | 28.805 | 35.647 | PHAGE_Gordon_Schwabeltier_NC_031255(1) | https://phaster.ca/submissions/ZZ_2f32f5ed66 | na | na | na | na | na | na | na | na r | na | na | |
| 2014017 | C. belfantii C. belfantii | negative | na | no | 8,8 | prophage | 53,8% | | e 20 | 6 | 49.348 | 58.178 | PHAGE_Rhodot_RM378_NC_004735(1) | https://phaster.ca/submissions/ZZ_2f32f5ed66 | na | na | na | na | na | na | na | na r | na | na | |
| 2014017 | C. belfantii C. belfantii | negative | na | no | 8,5 | prophage | 53,8% | | e 30 | 11 | 43.741 | 52.337 | PHAGE_Escher_D108_NC_013594(1) PHAGE_Rhodoc_REQ2_NC_016652(3) | https://phaster.ca/submissions/ZZ_2f32f5ed66 https://phaster.ca/submissions/ZZ_e084dae48c | na | na | na | na | na | na | na | na r | na | na | |
| 2015001 | C. belfantii | negative negative | na | no | 10.1 | prophage prophage | 53,7% 53,7% | | e 20 | 21 | 33.968 44.841 | 54 977 | PHAGE Mycoba Gardann NC 031124(3) | https://phaster.ca/submissions/ZZ_e084dae48c https://phaster.ca/submissions/ZZ_e084dae48c | na | na | na | na | na | na | na | na i | na na | na | |
| 2015001 | C. belfantii | negative | na | no | 24.2 | prophage | 53,7% | | e 10 | 32 | 2 | | PHAGE_Coryne_Poushou_NC_042139(8) | https://phaster.ca/submissions/ZZ_e084dae48c | na | na | na | na | na | na | na | na . | na | na | |
| 2015001 | C. belfantii | negative | na | no | 15.3 | prophage | 53,7% | 52,5% incomplet | e 10 | | 714 | | PHAGE Gordon Nyceirae NC 031004(8) | https://phaster.ca/submissions/ZZ_e084dae48c | na | na | na | na | na | na | na | na | na | na | |
| 2015167 | C. belfantii | negative | na | no | 10,9 | prophage | 53,7% | | e 10 | 15 | 78.147 | 89.111 | PHAGE_Escher_D108_NC_013594(1) | https://phaster.ca/submissions/ZZ_cc81808c40 | na | na | na | na | na | na | na | na | na | na | |
| 2015167 | C. belfantii | negative | na | no | 6,7 | prophage | 53,7% | | e 10 | 9 | 38.794 | | PHAGE_Gordon_Schwabeltier_NC_031255(1) | https://phaster.ca/submissions/ZZ_cc81808c40 | na | na | na | na | na | na | na | na | na | na | |
| 2015202 | C. belfantii | negative | na | no | 7,5 | prophage | 53,9% | | | 14 | 32.397 | 39.958 | PHAGE_Coryne_Poushou_NC_042139(2) | https://phaster.ca/submissions/ZZ_8c2e529f49 | na | na | na | na | na | na | na | na | na | na | |
| 2016001 | C. belfantii | negative | na | no | 18,3 | prophage | 53,8% | | ole 70 | 18 | 47.600 | | PHAGE_Gordon_GMA1_NC_030902(6) | https://phaster.ca/submissions/ZZ_e47c55be10 | na | na | na | na | na | na | na | na | na | na | |
| 2016007 | C. belfantii | negative | na | no | 6,8 | prophage | 53,7% | 54,9% incomplet | e 10 | 8 | 73.848 | | PHAGE_Gordon_Schwabeltier_NC_031255(1) | https://phaster.ca/submissions/ZZ_0f02a192f8 | na | na | na | na | na | na | na | na | na | na | |
| 2016007 | C. belfantii | negative | na | no | 10,9 | prophage | 53,7% | | e 10 | 16 | 322 | | PHAGE_Escher_D108_NC_013594(1) | https://phaster.ca/submissions/ZZ_0f02a192f8 | na | na | na | na | na | na | na | na | na | na | |
| 2016007 | C. belfantii | negative | na | no | 7,2 | prophage | 53,7% | | | 9 | 17.171 | | PHAGE_Synech_ACG_2014f_NC_026927(2) | https://phaster.ca/submissions/ZZ_0f02a192f8 | na | na | na | na | na | na | na | na | na | na | |
| 2016007 | C. belfantii | negative | na | no | 3,5 | prophage | 53,7% | | | 9 | 11.015 | | PHAGE_Bacter_Diva_NC_028788(1) | https://phaster.ca/submissions/ZZ_0f02a192f8 | na | na | na | na | na | na | na | na r | na | na | |
| 2017002 | C. belfantii | negative | na | no | 6,8 | prophage | 53,9% | | | 8 | 31.989 | | PHAGE_Gordon_Schwabeltier_NC_031255(1) | https://phaster.ca/submissions/ZZ_6e79231fb4 | na | na | na | na | na | na | na | na r | na | na | |
| 2017003 | C. belfantii | negative | na | no | 10,9 | prophage | 53,9% | | | 17 | 54.765 | | PHAGE_Mycoba_DrDrey_NC_022059(1) | https://phaster.ca/submissions/ZZ_6e79231fb4 | na | na | na | na | na | na | na | na r | na | na | |
| 2017004 | C. belfantii C. belfantii | negative | må | no | 10,2 | prophage | 53,9% | | e 10 | 7 | 1 | | PHAGE_Coryne_Poushou_NC_042139(6) | https://phaster.ca/submissions/ZZ_6e79231fb4 | na na | na | na | nd no | nd no | na na | na na | ne / | 70 | na | |
| 2017008 | C. belfantii C. belfantii | negative negative | na na | no | 10,2 | prophage | 53,7% 53,8% | | e 20 | | 78.238 | | PHAGE_Coryne_Poushou_NC_042139(9) | https://phaster.ca/submissions/ZZ_a20ef10933 https://phaster.ca/submissions/ZZ_f81d38bc7b | na na | na na | na na | na na | na na | na na | na na | na I | 70 | nd na | |
| 2018032 | C. belfantii | | na na | no | 6.8 | prophage prophage | 53,8% | | e 10 | | | 89.206 | PHAGE_Escher_D108_NC_013594(1) PHAGE_Gordon_Schwabeltier_NC_031255(1) | | na na | na na | na na | na na | na na | na na | na na | na I | na na | na na | |
| 2018032 | C. belfantii | negative negative | na | 00 | 7.9 | prophage | 53,8% | | e 10 | 8 | 28.433 | | PHAGE_Gordon_schwabettier_NC_031255(1) PHAGE_Coryne_Poushou_NC_042139(7) | https://phaster.ca/submissions/ZZ_f81d38bc7b https://phaster.ca/submissions/ZZ_f81d38bc7b | na | na | na | na | na | na | na | na | na | na | |
| 2018032 | C. belfantii | negative | na | no | 18.0 | prophage | 53,8% | | e 20 | 10 | 68.465 | 7.968 86.515 | PHAGE_Coryne_Poushou_NC_042139(7) PHAGE_Rhodoc_REQ3_NC_016654(6) | https://phaster.ca/submissions/ZZ_f81d38bc7b https://phaster.ca/submissions/ZZ_e5db0c7d55 | na | na | na | na | na | na | na | na | na | na | |
| 2018045 | C. belfantii | negative | na | no | 35,9 | prophage | 53,7% | | e 3/ | 9 17 | 00.465 | | PHAGE_Knodoc_KEQ3_NC_016654(6) PHAGE_Coryne_Poushou_NC_042139(11) | https://phaster.ca/submissions/ZZ_e5db0c7d55 https://phaster.ca/submissions/ZZ_e5db0c7d55 | na | na | na | na | na | na | na | na | na | na | |
| 2018048 | C. belfantii | negative | na | no | 13,7 | prophage | 53,7% | 55,0% incomplet | e 10 | 16 | 9.102 | | PHAGE Vibrio Ceto NC 042094(1) | https://phaster.ca/submissions/ZZ_62f7009629 | na | na | na | na | na | na | na | na | na | na | |
| 2018048 | C. belfantii | negative | na | no | 19,7 | prophage | 53,7% | | ole 70 | 20 | 25.890 | | PHAGE Rhodoc REQ3 NC 016654(6) | https://phaster.ca/submissions/ZZ_62(7009629 | na | na | na | na | na | na | na | na | na | na | |
| 2018076 | C. belfantii | negative | na | no | 20,7 | prophage | | 53,8% incomplet | e 20 | 14 | | | PHAGE_Coryne_Poushou_NC_042139(2) | https://phaster.ca/submissions/ZZ_2e2f19ce71 | na | na | na | na | na | na | na | na | na | na | |
| 2018076 | C. belfantii | negative | na | no | 27,3 | prophage | 53,7% | | | 36 | 23.010 | | PHAGE_Gordon_BritBrat_NC_030942(4) | https://phaster.ca/submissions/ZZ_2e2f19ce71 | na | na | na | na | na | na | na | na | na | na | |
| 2018077 | C. belfantii | negative | na | no | 15,3 | prophage | 53,7% | 52,5% incomplet | e 10 | 24 | | 15.376 | PHAGE_Gordon_Nyceirae_NC_031004(9) | https://phaster.ca/submissions/ZZ_2e2f19ce71 | na | na | na | na | na | na | na | na | na | na | |
| 2014016 | C. ulcerans | positive | positive | no | 6,8 | prophage | 53,3% | | | 8 | 28.436 | 35.277 | PHAGE_Gordon_Schwabeltier_NC_031255(1) | https://phaster.ca/submissions/ZZ_5d15ef0994 | na | na | na | na | na | na | na | na | na | na | |
| 2014017 | C. ulcerans | positive | positive | no | 10,9 | prophage | 53,3% | | | | 35.872 | 46.837 | PHAGE_Escher_D108_NC_013594(1) | https://phaster.ca/submissions/ZZ_5d15ef0994 | na | na | na | na | na | na | na | na | na | na | |
| 014018 | C. ulcerans | positive | positive | no | 6,3 | prophage | 53,3% | 59,0% incomplet | e 20 | 7 | 3.799 | | PHAGE_Gordon_Blueberry_NC_030943(2) | https://phaster.ca/submissions/ZZ_5d15ef0994 | na | na | na | na | na | na | na | na | na | na | |
| 014019 | C. ulcerans | positive | positive | no | 7,3 | prophage | 53,3% | | | 13 | 1 | 7.308 | PHAGE_Coryne_Poushou_NC_042139(7) | https://phaster.ca/submissions/ZZ_5d15el0994 | na | na | na | na | na | na | na | na | na | na | |
| 016002 | C. ulcerans | negative | na | no | 8,6 | prophage | 53,3% | | e 30 | 10 | 52.679 | 61.348 | PHAGE_Staphy_42E_NC_007052(1) | https://phaster.ca/submissions/ZZ_77058525d7 | na | na | na | na | na | na | na | na | na | na | |
| 017009 | C. ulcerans | positive | positive | no | 27,7 | prophage | 53,3% | | | | 2.329 | 30.095 | PHAGE_Clostr_phiCT453A_NC_028991(4) | https://phaster.ca/submissions/ZZ_f36f5315d2 | na | na | na | na | na | na | na | na | na | na | |
| 2017009 | C. ulcerans | positive | positive | no | 38,3 | prophage | 53,3% | | | 33 | | 38.947 | PHAGE_Gordon_Nyceirae_NC_031004(9) | https://phaster.ca/submissions/ZZ_f36f5315d2 | na | na | na | na | na | na | na | na r | na | na | |
| 2019012 | C. ulcerans | positive | positive | no | 19,2 | prophage | 53,4% | | e 60 | 19 | 209.532 | 228.818 | PHAGE_Gordon_GMA1_NC_030902(5) | https://phaster.ca/submissions/ZZ_9685ae8fc2 | na | na | na | na | na | na | na | na r | na | na | |
| 2019012 | C. ulcerans | positive | positive | no | 11,1 | prophage | 53,4% | | e 20 | | 232.087 | 243.192 | PHAGE_Mycoba_Che9c_NC_004683(1) | https://phaster.ca/submissions/ZZ_9685ae8fc2 | na | na | na | na | na | na | na | na / | na | na | |
| 2019012 | C. ulcerans C. diphtheriae | positive | positive | no | 35,6 19.6 | prophage | 53,4% | | e 40 | | 190 | 35.873 | PHAGE_Gordon_Nyceirae_NC_031004(10) PHAGE_Gordon_GMA1_NC_030902(7) | https://phaster.ca/submissions/ZZ_9685ae8fc2 | na | na | na | na | na | na | na | na r | na | na | |
| 2014018 | C. diphtheriae C. diphtheriae | positive positive | positive positive | no | 15.2 | prophage | 53,6% | | e 30 | 19 | 20.720 | | PHAGE_Rhodoc_REQ3_NC_016654(2) | https://phaster.ca/submissions/ZZ_626e2bb32c | na | na | na | na | na | na | na | na i | na na | na | |
| 2014019 | C. diphtheriae | positive | positive | no | 33.6 | prophage prophage | 53,6% 53,6% | | e 30 | 25 | | 58.758 | PHAGE_Coryne_Poushou_NC_042139(9) | https://phaster.ca/submissions/ZZ_626e2bb32c https://phaster.ca/submissions/ZZ_626e2bb32c | na | na | na | na | na | na | na | na i | na na | na | |
| 2014021 | C. diphtheriae | positive | positive | 00 | 17.7 | prophage | 53,6% | | 0 10 | 20 | 219.353 | 17 707 | PHAGE Coryne Poushou NC 042139(6) | https://phaster.ca/submissions/ZZ_626e2bb32c | na | na | na | na | na | na | na | na | na | na | |
| 2015002 | C. diphtheriae | negative | na | no | 6.7 | prophage | 53,5% | 55,2% incomplet | e 10 | 8 | 35.538 | | PHAGE_Gordon_Schwabeltier_NC_031255(1) | https://phaster.ca/submissions/ZZ_d7a02c623d | na | na | na | na | na | na | na | ina | na | na | |
| 2015002 | C. diphtheriae | negative | na | no | 8.6 | prophage | 53,5% | | e 10 | 13 | | | PHAGE Synech S SSM7 NC 015287(1) | https://phaster.ca/submissions/ZZ_d7a02c623d | na | na | na | na | na | na | na | ina | na | na | |
| 2015002 | C. diphtheriae | negative | na | no | 5.2 | prophage | 53,5% | | e 30 | 8 | 3 | 5.255 | PHAGE_Rhodot_RM378_NC_004735(1) | https://phaster.ca/submissions/ZZ_d7a02c623d | na | na | na | na | na | na | na | na | na | na | |
| 2015004 | C. diphtheriae | positive | positive | no | 23,1 | prophage | 53,5% | | | 25 | 1.139 | | PHAGE_Gordon_Nyceirae_NC_031004(7) | https://phaster.ca/submissions/ZZ 8e8f9fe4a | na | na | na | na | na | na | na | na | na | na | |
| 2015004 | C. diphtheriae | negative | na | no | 15,1 | prophage | 53,5% | 53,3% intact | 96 | 5 14 | 13.308 | 28.410 | PHAGE_Coryne_phi674_NC_042355(10) | https://phaster.ca/submissions/ZZ_8e8f9fe4a | na | na | na | na | na | na | na | na | na | na | |
| 2016005 | C. diphtheriae | negative | na | no | 6,7 | prophage | 53,4% | 55,2% incomplet | e 10 | 8 | 54.536 | | PHAGE_Gordon_Schwabeltier_NC_031255(1) | https://phaster.ca/submissions/ZZ 2992c68305 | na | na | na | na | na | na | na | na | na | na | |
| 2016005 | C. diphtheriae | negative | na | no | 8,6 | prophage | 53,4% | 55,8% incomplet | e 10 | 14 | 17.045 | | PHAGE_Synech_S_SSM7_NC_015287(1) | https://phaster.ca/submissions/ZZ_2992c68305 | na | na | na | na | na | na | na | na | na | na | |
| 2016005 | C. diphtheriae | negative | na | no | 5,8 | prophage | 53,4% | | | 8 | 245 | 6.076 | PHAGE_Rhodot_RM378_NC_004735(1) | https://phaster.ca/submissions/ZZ_2992c68305 | na | na | na | na | na | na | na | na r | na | na | |
| 2016006 | C. diphtheriae | positive | positive | no | 13,8 | prophage | 53,6% | | | 20 | 35.134 | 48.970 | PHAGE_Rhodoc_REQ3_NC_016654(2) | https://phaster.ca/submissions/ZZ_c2b91f0b16 | na | na | na | na | na | na | na | na r | na | na | |
| 2016006 | C. diphtheriae | positive | positive | no | 18,0 | prophage | 53,6% | | | | 52.796 | | PHAGE_Gordon_GMA1_NC_030902(7) | https://phaster.ca/submissions/ZZ_c2b91f0b16 | na | na | na | na | na | na | na | na r | na | na | |
| 016006 | C. diphtheriae | positive | positive | no | 28.0 | prophage | 53,6% | | 110 | | 2.058 | 38.360 | | https://phaster.ca/submissions/ZZ_c2b91f0b16 | na | na | na | na | na | na | na | na r | na | na | |
| 1016006 | C. diphtheriae C. diphtheriae | positive | positive | no | 46.4 | prophage | 53,6% | | | | 41.032 | 69.121 | PHAGE_Coryne_Poushou_NC_042139(9) PHAGE_Gordon_Attis_NC_041883(4) | https://phaster.ca/submissions/ZZ_c2b91f0b16 https://phaster.ca/submissions/ZZ_67f6e68788 | na na | na | na na | na na | na | na na | na na | na I | na na | na na | |
| 2017001 | C. diphtheriae C. diphtheriae | negative negative | na | 00 | 27.5 | prophage prophage | 53,6% 53,2% | 55,2% incomplet | e 60 96 | 63 | 98 2.641 | 40.547 | PHAGE_Gordon_Attis_NC_041883(4) PHAGE_Coryne_phi674_NC_042355(10) | | na . | na | na | na | na na | na | na | na / | na na | na na | |
| 2017004 | C. diphtheriae | negative | na | no | 35.5 | prophage | 53,2% | | 110 | | 19.374 | 54.939 | PHAGE_Coryne_phi674_NC_042355(10) PHAGE_Coryne_phi674_NC_042355(11) | https://phaster.ca/submissions/ZZ_aeda932eb6 https://phaster.ca/submissions/ZZ_5bcfc8bb4Z | na | na | na | na | na | na | na | ina i | na | na | |
| 2017014 | C. diphtheriae | positive | negative | no | 17,2 | prophage | 53,5% | | | | 44.306 | 61.526 | PHAGE Coryne Poushou NC 042139(3) | https://phaster.ca/submissions/ZZ_bck.86642 https://phaster.ca/submissions/ZZ_b4a7b57190 | na | na | na | na | na | na | na | na | na | na | |
| 017015 | C. diphtheriae | negative | na | no | 23,3 | prophage | 53,8% | | e 40 | 31 | 68.603 | 91.907 | PHAGE_Gordon_GMA1_NC_030902(7) | https://phaster.ca/submissions/ZZ 9310f16523 | na | na | na | na | na | na | na | na | na | na | |
| 017015 | C. diphtheriae | negative | na | no | 13,4 | prophage | 53,8% | | e 30 | 20 | 92.787 | 106.238 | PHAGE_Rhodoc_REQ3_NC_016654(2) | https://phaster.ca/submissions/ZZ 9310f16523 | na | na | na | na | na | na | na | na | na | na | |
| 017015 | C. diphtheriae | negative | na | no | 24,9 | prophage | 53,8% | 55,4% incomplet | e 20 | 32 | 8.063 | 32.965 | PHAGE_Gordon_Attis_NC_041883(4) | https://phaster.ca/submissions/ZZ 9310f16523 | na | na | na | na | na | na | na | na | na | na | |
| 017016 | C. diphtheriae | negative | na | no | 20,8 | prophage | 53,7% | 55,7% incomplet | e 40 | 23 | 94.165 | 115.027 | PHAGE_Gordon_GMA1_NC_030902(7) | https://phaster.ca/submissions/ZZ_df549e467d | na | na | na | na | na | na | na | na | na | na | |
| 017016 | C. diphtheriae | negative | na | no | 34,9 | prophage | 53,7% | 53,8% incomplet | e 20 | 39 | 215.141 | 250.084 | PHAGE_Gordon_Nyceirae_NC_031004(8) | https://phaster.ca/submissions/ZZ_df549e467d | na | na | na | na | na | na | na | na | na | na | |
| 2017016 | C. diphtheriae | negative | na | no | 43,4 | prophage | 53,7% | 55,4% incomplet | e 50 | 48 | 196.829 | | PHAGE_Coryne_Poushou_NC_042139(10) | https://phaster.ca/submissions/ZZ_df549e467d | na | na | na | na | na | na | na | na | na | na | |
| 017017 | C. diphtheriae | negative | na | no | 15,0 | prophage | 53,6% | | e 10 | 23 | 37.774 | | PHAGE_Arthro_Colucci_NC_042000(2) | https://phaster.ca/submissions/ZZ_d92c62cbb3 | na | na | na | na | na | na | na | na | na | na | |
| 2017017 | C. diphtheriae | negative | na | no | 19,3 | prophage | 53,6% | 56,2% incomplet | e 30 | 20 | 55.230 | | PHAGE_Gordon_GMA1_NC_030902(6) | https://phaster.ca/submissions/ZZ_d92c62cbb3 | na | na | na | na | na | na | na | na | na | na | |
| 017017 | C. diphtheriae | negative | na | no | 32,4 | prophage | 53,6% | | | | | | PHAGE_Coryne_Poushou_NC_042139(9) | https://phaster.ca/submissions/ZZ_d92c62cbb3 | na | na | na | na | na | na | na | na | na | na | |
| 017018 | C. diphtheriae | negative | na | no | 15,0 | prophage | 53,6% | | | 23 | 37.774 | | PHAGE_Arthro_Colucci_NC_042000(2) | https://phaster.ca/submissions/ZZ_544ba92965 | na | na | na | na | na | na | na | na r | na | na | |
| 017018 | C. diphtheriae | negative | ná | no | 19,3 | prophage | 53,6% | | | | 55.230 | 74.605 | PHAGE_Gordon_GMA1_NC_030902(6) | https://phaster.ca/submissions/ZZ_544ba92965 | na | na | na | ná | ná | na | na | na / | na . | na | |
| 017018 | C. diphtheriae | negative | ná | no | 32,4 | prophage | 53,6% | | | 28 | 1 | 32.435 | PHAGE_Coryne_Poushou_NC_042139(9) | https://phaster.ca/submissions/ZZ_544ba92965 | na | na | na | ná | ná | na | na | na P | na . | ria | |
| 017042 | C. diphtheriae C. diphtheriae | negative | na | no | 14,2 | prophage | 53,7% | | | | | 31.006 | PHAGE_Rhodoc_RRH1_NC_016651(8) | https://phaster.ca/submissions/ZZ_c29af5d025 | na na | na | na | na | na | na | na | na / | na na | na na | |
| 017043 | C. diphtheriae | negative negative | na | 00 | 25.7 | prophage prophage | 53,4% 53,4% | | | 20 | 37.427 62.244 | 51.889 | PHAGE_Mycoba_Spartacus_NC_041986(2) PHAGE_Coryne_Poushou_NC_042139(11) | https://phaster.ca/submissions/ZZ_e185c9129d https://phaster.ca/submissions/ZZ_e185c9129d | na | na | na | na | na | na | na | na l | na | na | |
| 017043 | C. diphtheriae | negative | na | 00 | 14.2 | prophage | 53,4% | | | 25 | 62.244 44.061 | 87.958 59.306 | PHAGE_Coryne_Poushou_NC_042139(11) PHAGE_Rhodoc_RRH1_NC_016651(8) | https://phaster.ca/submissions/ZZ_e185c9129d https://phaster.ca/submissions/ZZ_e185c9129d | na | na | na | na | na | na | na | na / | na | na | |
| 017045 | C. diphtheriae | negative | na | no | 9.5 | prophage | 53,4% | 56.7% incomplet | e 10 | | 17.113 | 26.290 | PHAGE_Staphy_StauST398_2_NC_021323(1) | https://phaster.ca/submissions/ZZ_e185c91290 https://phaster.ca/submissions/ZZ_649bbe74c8 | na | na | na | na | na | na | na | na ' | na | na | |
| 017046 | C. diphtheriae | negative | na | no | 6.7 | prophage | 53,4% | | e 10 | 2 2 | 71.648 | 78 429 | PHAGE_Gordon_Schwabeltier_NC_031255(1) | https://phaster.ca/submissions/ZZ_649bbe74c8 | na | na | na | na | na | na | na | na | na | na | |
| 017046 | C. diphtheriae | negative | na | no | 8,8 | prophage | | 51,6% incomplet | e 60 | 13 | 72.040 | 8,850 | PHAGE_Plankt_PaV_LD_NC_016564(1) | https://phaster.ca/submissions/ZZ_649bbe74c8 | na | na | na | na | na | na | na | na | na | na | |
| 017047 | C. diphtheriae | negative | na | no | 39,6 | prophage | 53,5% | 52,3% incomplet | e 20 | 35 | 39.866 | 79.554 | PHAGE_Gordon_Nyceirae_NC_031004(8) | https://phaster.ca/submissions/ZZ_65cc2340f7 | na | na | na | na | na | na | na | na | na | na | |
| 017047 | C. diphtheriae | negative | na | no | 10,9 | prophage | 53,5% | | e 20 | 21 | 123.930 | | PHAGE Synech_S_SSM7_NC_015287(1) | https://phaster.ca/submissions/ZZ_65cc2340f7 | na | na | na | na | na | na | na | na | na | na | |
| 019026 | C. diphtheriae | negative | na | no | 6,7 | prophage | 53,5% | 55,2% incomplet | e 10 | 8 | 99.152 | 105.933 | PHAGE_Gordon_Schwabeltier_NC_031255(1) | https://phaster.ca/submissions/ZZ_a710b92d27 | na | na | na | na | na | na | na | na | na | na | |
| 019026 | C. diphtheriae | negative | na | no | 12,5 | prophage | 53,5% | 53,6% incomplet | e 40 | 10 | 140.864 | 153.374 | PHAGE_Rhodot_RM378_NC_004735(1) | https://phaster.ca/submissions/ZZ_a710b92d27 | na | na | na | na | na | na | na | na | na | na | |
| 019026 | C. diphtheriae | negative | na | no | 8,6 | prophage | 53,5% | | e 10 | 13 | | | PHAGE_Synech_5_SSM7_NC_015287(1) | https://phaster.ca/submissions/ZZ_a710b92d27 | na | na | na | na | na | na | na | na | na | na | |
| | C. diphtheriae | positive | positive | no | 32,8 | prophage | 53,6% | 53,0% intact | 110 | | 245.470 | 278.302 | PHAGE_Coryne_phi674_NC_042355(10) | https://phaster.ca/submissions/ZZ_8ca43a6a60 | na | na | na | na | na | na | na | na | na | na | |
| 019027 | | negative | na | no | 6,7 | prophage | 53,5% | | | | 99.090 | 105.872 | PHAGE_Gordon_Schwabeltier_NC_031255(1) | https://phaster.ca/submissions/ZZ_279260358f | na | na | na | na | na | na | na | na | na | na | |
| 2019027 2019028 | C. diphtheriae | | | | | | | | | | | | | | $\overline{}$ | | | | | | | | | | |
| 2019028 2019028 | C. diphtheriae C. diphtheriae | negative | na | no | 8,6 | prophage | 53,5% | 55,8% incomplet | e 10 | 13 | 70.286 | | PHAGE_Synech_S_SSM7_NC_015287(1) | https://phaster.ca/submissions/ZZ 279260358f | na | na | na | na | na | na | na | na | na | na | |
| 2019028 2019028 2019028 | | negative negative | na na positive | no no | 8,6 5,8 35,4 | prophage prophage prophage | 53,5% | 55,8% incomplet 53,9% incomplet 52,6% incomplet | e 30 | 8 | 4.623 | 10.454 | PHAGE_Synech_5_SSM7_NC_015287(1) PHAGE_Rhodot_RM378_NC_004735(1) PHAGE_Coryne_Poushou_NC_042139(11) | https://phaster.ca/submissions/ZZ_279260358f https://phaster.ca/submissions/ZZ_279260358f https://phaster.ca/submissions/ZZ_b6bf52cac3 | na | na na | na | na na | na | na na | na na | na n | na na | na na | |